



# CLUSTAL 2.0.5 multiple sequence alignment

```

gi|45825280|gb|AAS77488.1|          MVYFLNFMSTINVPVLKRARLYMATNRLLVVVLVVLLVWTVQNVWTWSPG 50
gi|150864372|ref|XP_001383155.    -----MINKRVLRLGLIAVLVLYLYGFFRTFSVPGSSHRTES 37
VIRT19386|VIRT19386                -----MAKADGSLLYNPHNPPRRYFYFMAIFAVSIVCVLYGP 38
gi|1322520|emb|CAA96740.1|        -----MSRKLSHLIATRSKRTIVVTVLLIYSLLTFHLNKRLLSQF 41
                                     .: * : * * *

gi|45825280|gb|AAS77488.1|          TRDLAQVDAKIEAELNSNLHTFGAHLRHLNRLPAESATLREKILTFYFPYY 100
gi|150864372|ref|XP_001383155.    SSSKLQLKRELEITHSNWAKTG-LNFQPNKKARLP IETTVRQQLSFQFPYE 86
VIRT19386|VIRT19386                SSQLSSPKIDYDPLTILRSIDLKYLEAPSQLSPGITVEDNLRQLFEFFPYR 88
gi|1322520|emb|CAA96740.1|        YPSKDDFKQTLILPTTSHSQDINLKQITVNKKQNQLNLELDQLSFAPPYD 91
                                     .: * : * * *

gi|45825280|gb|AAS77488.1|          PEKVPDNQIWQTKVKVDLEDDNFPKQYRRFQKTWV-EKNPDYVYHLIPDSV 149
gi|150864372|ref|XP_001383155.    SSKEPQKNIWQTKWVALDDDSFPLKYRTYQSTWD-DKNPGYKHYVVADDV 135
VIRT19386|VIRT19386                SYEPFPQHIWQTKVSPSDSSFPKNFKDLGESWL-QRSPNYDHFVIPDDA 137
gi|1322520|emb|CAA96740.1|        SQAPIQRVWQTKWKVGADDDKNPSSFRITYQKTWSGSYSFDYQYSLISDDS 141
                                     . * .: : ***** . . . . . * .: : * .: : * .: : * .: : *

gi|45825280|gb|AAS77488.1|          IEDFVASIYANVPEVVAYQLLPKNIMKADFFRYLYVIYARGGYSDDMTV 199
gi|150864372|ref|XP_001383155.    CEELISQLYSTVPDVARAYNIMPKSILKADFFRYLILYARGGVYSDIDTV 185
VIRT19386|VIRT19386                AWELIHHEYERVFEVLEAFHLLPEPILKADFFRYLILFARGGLYADMDTM 187
gi|1322520|emb|CAA96740.1|        IIPFLENLIYAPVPVIVIQAFKLMPCNILKADFLRYLLLFARGGIYSDMDTM 191
                                     :: * * * * .: : : : * * : * * * * : * * * * * * * * * * * *

gi|45825280|gb|AAS77488.1|          CLKPIKDWATFDRDLIHAADNKADLS-----QIDFEARTTPVGLVIG 241
gi|150864372|ref|XP_001383155.    GLKPIDKWVSSNTILYDKPINP-----GLVVG 212
VIRT19386|VIRT19386                LLKPTESWLTFNETIGGVKNAG-----LVIG 214
gi|1322520|emb|CAA96740.1|        LLKPIDSWPSQNKSWLNIIIDLNKPIPYKNSKPSLLSSDEISHQPGLVIG 241
                                     ***** * : : : : : : : : : : : : : : : * * : *

gi|45825280|gb|AAS77488.1|          IEADPRDPDWHWFRRRLQFCQWTIQAKPGHPLLRELLIRIVEETFRKQH 291
gi|150864372|ref|XP_001383155.    IEADDRDPDWAERYARRIQFCQWTIQAKKGHPMLRELIATITEKTLTRAR 262
VIRT19386|VIRT19386                IEADDRDPDWDHWYARRIQFCQWAIQSKRGHPALRELIVRVVSTTLRKEK 264
gi|1322520|emb|CAA96740.1|        IEADDRDDWSEWYARRIQFCQWTIQAKPGHPILRELLINITATTLASVQ 291
                                     ***** * * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

gi|45825280|gb|AAS77488.1|          -----MGVLKRVEGKDSGADIMQ 309
gi|150864372|ref|XP_001383155.    -----KGQLKKVLGKDEGGDIMN 280

```

